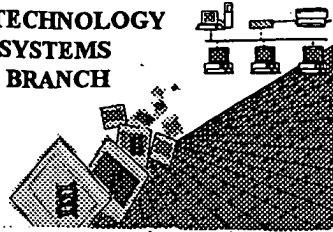


**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0590  
03061636  
**RECEIVED**

MAR 19 2002

TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/941,193  
Source: 1636  
Date Processed by STIC: 3/1/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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## Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/941,193

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics  
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino  
Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0  
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences  
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(ix) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences  
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ **Use of n's or Xaa's  
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>  
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0  
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001



1636

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/941,193

DATE: 03/01/2002  
TIME: 14:45:45

Input Set : A:\Seq-sub.app  
Output Set: N:\CRF3\03012002\I941193.raw

**Does Not Comply  
Corrected Diskette Needed**

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: BROW, MARY ANN D.  
7 LYAMICHEV, VICTOR I.  
8 OLIVE, DAVID M.  
10 (ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF  
11 PATHOGENS  
13 (iii) NUMBER OF SEQUENCES: 165  
15 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: MEDLEN & CARROLL  
17 (B) STREET: 220 MONTGOMERY STREET, SUITE 2200  
18 (C) CITY: SAN FRANCISCO  
19 (D) STATE: CALIFORNIA  
20 (E) COUNTRY: UNITED STATES OF AMERICA  
21 (F) ZIP: 94104  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
29 (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER: US/09/941,193  
31 (B) FILING DATE: 28-Aug-2001  
32 (C) CLASSIFICATION:  
34 (viii) ATTORNEY/AGENT INFORMATION:  
35 (A) NAME: CARROLL, PETER G.  
36 (B) REGISTRATION NUMBER: 32,837  
37 (C) REFERENCE/DOCKET NUMBER: FORS-01756  
39 (ix) TELECOMMUNICATION INFORMATION:  
40 (A) TELEPHONE: (415) 705-8410  
41 (B) TELEFAX: (415) 397-8338

## ERRORED SEQUENCES

44 (2) INFORMATION FOR SEQ ID NO: 1:  
46 (i) SEQUENCE CHARACTERISTICS:  
47 (A) LENGTH: 2506 base pairs  
48 (B) TYPE: nucleic acid  
49 (C) STRANDEDNESS: double  
50 (D) TOPOLOGY: linear  
52 (ii) MOLECULE TYPE: DNA (genomic)  
56 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

PP. 2-3

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/941,193

DATE: 03/01/2002  
TIME: 14:45:45

Input Set : A:\Seq-sub.app  
Output Set: N:\CRF3\03012002\I941193.raw

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E--> 58 ATGAGGGGGA TGCTGCCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT
59 GGACGGCCAC 60
E--> 61 CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG
62 GGGGGAGCCG 120
E--> 64 GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA
65 GGACGGGGAC 180
E--> 67 GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC
68 CTACGGGGGG 240
E--> 70 TACAAGGCGG GCCGGGCCCC CACGCCGGAG GACTTTCCCC GGCAACTCGC
71 CCTCATCAAG 300
E--> 73 GAGCTGGTGG ACCTCCTGGG GCTGGCGCGC CTCGAGGTCC CGGGCTACGA
74 GCGCGACGAC 360
E--> 76 GTCCTGGCCA GCCTGGCCAA GAAGGCGGAA AAGGAGGGCT ACGAGGTCCG
77 CATCCTCACC 420
E--> 79 GCCGACAAAG ACCTTTACCA GTCCTTTTCC GACCGCATCC ACGTCCTCCA
80 CCCCAGAGGG 480
E--> 82 TACCTCATCA CCCC GGCCCTG GCTTTGGGAA AAGTACGGCC TGAGGCCCGA
83 CCACTGGGCC 540
E--> 85 GACTACCGGG CCCTGACCGG GGACGAGTCC GACAACCTTC CCGGGGTCAA
86 GGGCATCGGG 600
E--> 88 GAGAAGACGG CGAGGAAGCT TCTGGAGGAG TGGGGGAGCC TGGGAAGCCCT
89 CCTCAAGAAC 660
E--> 91 CTGGACCGGC TGAAGCCCGC CATCCGGGAG AAGATCCTGG CCCACATGGA
92 CGATCTGAAG 720
E--> 94 CTCTCCTGGG ACCTGGCCAA GGTGCGCACC GACCTGCCCC TGGAGGTGGA
95 CTTGCGCCAA 780
E--> 97 AGGCGGGAGC CCGACCGGGA GAGGCTTAGG GCCTTTCTGG AGAGGCTTGA
98 GTTTGGCAGC 840
E--> 100 CTCCTCCACG AGTTGCGCCT TCTGGAAAGC CCCAAGGCC TGGAGGAGGC
101 CCCCTGGCCC 900
E--> 103 CCGCCGGAAG GGGCCTTCGT GGGCTTTGTG CTTTCCCGCA AGGAGCCCAT
104 GTGGGCCGAT 960
E--> 106 CTTCTGGCCC TGGCCGCCG CAGGGGGGGC CGGGTCCACC GGGCCCCCGA
107 GCCTTATAAA 1020
E--> 109 GCCCTCAGGG ACCTGAAGGA GCGCGGGGG CTTCTCGCCA AAGACCTGAG
110 CGTTCTGGCC 1080
E--> 112 CTGAGGGAAG GCCTTGGCCT CCCGCCCGG GACGACCCCA TGCTCCTCGC
113 CTACCTCCTG 1140
E--> 115 GACCCTTCCA ACACCACCCC CGAGGGGGTG GCCC GGCGCT ACGGCGGGGA
116 GTGGACGGAG 1200
E--> 118 GAGGCGGGGG AGCGGGCCGC CTTTCCGAG AGGCTCTTCG CCAACCTGTG
119 GGGGAGGCTT 1260
E--> 121 GAGGGGGAGG AGAGGCTCCT TTGGCTTTAC CGGGAGGTGG AGAGGCCCCCT
122 TTCCGCTGTC 1320
E--> 124 CTGGCCACCA TGGAGGCCAC GGGGGTGCGC CTGGACGTGG CCTATCTCAG
125 GCCTTGTC 1380
E--> 127 CTGGAGGTGG CCGAGGAGAT CGCCCGCCTC GAGGCCGAGG TCTTCCGCCT
128 GGCCGGCCAC 1440
E--> 130 CCCTTCAACC TCAACTCCCG GGACCAGCTG GAAAGGGTCC TCTTTGACGA

```

*global format  
error*

*see item 1 on  
Error summary sheet*

*Due to size  
of Sequence Listing,  
these pages only, is  
shown as a sample  
of global error.*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/941,193

DATE: 03/01/2002  
TIME: 14:45:45

Input Set : A:\Seq-sub.app  
Output Set: N:\CRF3\03012002\I941193.raw

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131 GCTAGGGCTT      1500
E--> 133 CCCGCCATCG GCAAGACGGA GAAGACCGGC AAGCGCTCCA CCAGCGCCGC
134 CGTCCTGGAG      1560
E--> 136 GCCCTCCGCG AGGCCCCACCC CATCGTGGAG AAGATCCTGC AGTACCGGGA
137 GCTCACCAAG      1620
E--> 139 CTGAAGAGCA CCTACATTGA CCCCTTGCCG GACCTCATCC ACCCCAGGAC
140 GGGCCGCCTC      1680
E--> 142 CACACCCGCT TCAACCAGAC GGCCACGGCC ACGGGCAGGC TAAGTAGCTC
143 CGATCCCAAC      1740
E--> 145 CTCCAGAACA TCCCCGTCCG CACCCCGCTT GGGCAGAGGA TCCGCCGGGC
146 CTTTCATCGCC      1800
E--> 148 GAGGAGGGGT GGCTATTGGT GGCCCTGGAC TATAGCCAGA TAGAGCTCAG
149 GGTGCTGGCC      1860
E--> 151 CACCTCTCCG GCGACGAGAA CCTGATCCGG GTCTTCCAGG AGGGGCGGGA
152 CATCCACACG      1920
E--> 154 GAGACGCCCA GCTGGATGTT CGGCGTCCCC CGGGAGGCCG TGGACCCCTT
155 GATGCGCCGG      1980
E--> 157 GCGGCCAAGA CCATCAACTT CGGGGTCCCTC TACGGCATGT CGGCCACCG
158 CCTCTCCCAG      2040
E--> 160 GAGCTAGCCA TCCCTTACGA GGAGGCCAG GCCTTCATTG AGCGCTACTT
161 TCAGAGCTTC      2100
E--> 163 CCCAAGGTGC GGGCCTGGAT TGAGAAGACC CTGGAGGAGG GCAGGAGGCG
164 GGGGTACGTG      2160
E--> 166 GAGACCTCTT TCGGCCGCCG CCGCTACGTG CCAGACCTAG AGGCCCGGGT
167 GAAGAGCGTG      2220
E--> 169 CGGGAGGCGG CCGAGCGCAT GGCCTTCAAC ATGCCCGTCC AGGGCACCGC
170 CGCCGACCTC      2280
E--> 172 ATGAAGCTGG CTATGGTGAA GCTCTTCCCC AGGCTGGAGG AAATGGGGGC
173 CAGGATGCTC      2340
E--> 175 CTTTCAGGTCC ACGACGAGCT GGTCTCGAG GCCCAAAAAG AGAGGGCGGA
176 GGCCGTGGCC      2400
E--> 178 CGGCTGGCCA AGGAGGTCAT GGAGGGGGTG TATCCCCTGG CCGTGCCCCT
179 GGAGGTGGAG      2460
E--> 181 GTGGGGATAG GGGAGGACTG GCTCTCCGCC AAGGAGTGAT ACCACC
W--> 182 2506
184 (2) INFORMATION FOR SEQ ID NO: 2:
186 (i) SEQUENCE CHARACTERISTICS:
187 (A) LENGTH: 2496 base pairs
188 (B) TYPE: nucleic acid
189 (C) STRANDEDNESS: double
190 (D) TOPOLOGY: linear
192 (ii) MOLECULE TYPE: DNA (genomic)
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 198 ATGGCGATGC TTCCCCTCTT TGAGCCCAAA GGCCGCGTGC TCCTGGTGGA
199 CGGCCACCAC      60
E--> 201 CTGGCCTACC GCACCTTCTT TGCCCTCAAG GGCCTACCA CCAGCCGCGG
202 CGAACCCGTT      120
E--> 204 CAGGCGGTCT ACGGCTTCGC CAAAAGCCTC CTCAAGGCCC TGAAGGAGGA
205 CGGGGACGTG      180

```

*see item 1*

*see item 1*